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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Leonard Guarente et al. Art Unit : 1645
Serial No. : 09/461,580 Examiner : R. Zeman
Filed : December 15, 1999
Title : METHODS FOR IDENTIFYING AGENTS WHICH ALTER HISTONE
 PROTEIN ACETYLATION, DECREASE AGING, INCREASE LIFESPAN

BOX SEQUENCE

U.S. Patent and Trademark Office
P.O. Box 2327
Arlington, VA 22202

RESPONSE TO NOTICE TO COMPLY WITH REQUIREMENTS
FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE AND/OR AMINO ACID SEQUENCES

In response to the communication dated August 15, 2002 (copy enclosed), applicants submit herewith a Sequence Listing in computer-readable form as required by 37 CFR §1.824. In addition, applicants submit a substitute Sequence Listing as required under 37 CFR §1.823(a) and a statement under 37 CFR §1.821(f).

Applicants respectfully request entry of the paper copy and computer-readable copy of the Sequence Listing filed herewith for the instant application. Furthermore, applicants request entry of the following amendments.

In the specification:

Replace the original Sequence Listing with the substitute Sequence Listing filed herewith.

CERTIFICATE OF MAILING BY FIRST CLASS MAIL

I hereby certify under 37 CFR §1.8(a) that this correspondence is being deposited with the United States Postal Service as first class mail with sufficient postage on the date indicated below and is addressed to the U.S. Patent and Trademark Office, P.O. Box 2327, Arlington, VA 22202.

September 11, 2002

Date of Deposit

Signature

Cassandra Beepot

Cassandra Beepot

Typed or Printed Name of Person Signing Certificate

Replace the paragraph beginning at page 63, line 4 with the following rewritten paragraph:

E) TBLASTN searches were performed on the NCBI mouse EST sequence databases, using the amino acid sequence of ySir2p. All mouse EST sequences homologous to ySir2p were classified into three groups termed α , β , and γ , based on the homology results from the searches. Three representative EST cDNA clones were purchased for three mouse homolog groups from Genome Systems Inc (St. Louis, MO): AA199012 for α , AA105536 for β , and AA260334 for γ . The cDNA clones were partially or completely sequenced. All deduced amino acid sequences were aligned with the Clustal X program. To cover each core domain completely, amino acid sequences of AA137380 and AA212772 for β and γ respectively, were also used. A phylogenetic tree of the core domains of the yeast and mouse *Sir2* families was generated with the Clustal X and NJPLOT program by using the following amino acid sequences: position 228-499 for ySir2p, 174-440 for yHst1p, 1-251 for yHst2p, 26-315 for yHst3p, 65-343 for yHst4, 215-460 for mSir2 α , TLGL (SEQ ID NO:36) to LINKEK (SEQ ID NO:32) for mSir2 β , and FG GG (SEQ ID NO:37) to LINRDL (SEQ ID NO:33) for mSIR2 γ .